WEST Search History

| Hide Items | Restore | Clear | Cancel |

DATE: Tuesday, July 25, 2006

Hide?	Set Name	Query	Hit Count
		DB=PGPB,USPT,EPAB,JPAB,DWPI; THES=ASSIGNEE; PLUR=NO; OP=ADJ	
☐	L6	(((ailim or icos or 8f4 or jtt$ or crp1 or crp-1) not icos.as.) with inflammat$).clm.	1
☐	L5	((ailim or icos or 8f4 or jtt$ or crp1 or crp-1) not icos.as.) with inflammat$	54
☐	L4	((ailim or icos or 8f4 or jtt$ or crp1 or crp-1) not icos.as.) same inflammat$	127
☐	L3	((ailim or icos or 8f4 or jtt$ or crp1 or crp-1) not icos.as.) and inflammat$	1029
☐	L2	(((ailim or icos or 8f4 or jtt$ or crp1 or crp-1) not icos.as.) and (tamatani-t$ or tezuka-k$).in.)	27
		DB=PGPB,USPT; THES=ASSIGNEE; PLUR=NO; OP=ADJ	
☐	L1	(((ailim or icos or 8f4 or jtt$ or crp1 or crp-1) not icos.as.) and (tamatani-t$ or tezuka-k$).in.)	19

END OF SEARCH HISTORY

,

SCORE Search Results Details for Application 10723602 and Search Result us-10-723-602-2.rag.

| Score Home Page | Retrieve Application List | SCORE System Overview | SCORE FAQ | Comments / Suggestions |

This page gives you Search Results detail for the Application 10723602 and Search Result us-10-723-602-2.rag.

start

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OM protein - protein search, using sw model

Run on: May 26, 2006, 11:11:28 ; Search time 431.325 Seconds
                                          (without alignments)
                                          210.945 Million cell updates/sec

Title: US-10-723-602-2
Perfect score: 1082
Sequence: 1 MKSGLWYFFLFCLRIKVLTG..........YMFMRAVNTAKKSRLTDVTL 199

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   A_Geneseq_8:*
                 1: geneseqp1980s:*
                 2: geneseqp1990s:*
                 3: geneseqp2000s:*
                 4: geneseqp2001s:*
                 5: geneseqp2002s:*
                 6: geneseqp2003as:*
                 7: geneseqp2003bs:*
                 8: geneseqp2004s:*
                 9: geneseqp2005s:*
                 10: geneseqp2006s:*

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.

SUMMARIES

SCORE Search Results Details for Application 10723602 and Search Result us-10-723-602-2.rai.

This page gives you Search Results detail for the Application 10723602 and Search Result us-10-723-602-2.rai.

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```
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OM protein - protein search, using sw model

Run on:        May 26, 2006, 11:27:41 ; Search time 90.4545 Seconds
                                        (without alignments)
                                        192.567 Million cell updates/sec

Title:         US-10-723-602-2
Perfect score: 1082
Sequence:      1 MKSGLWYFFLFCLRIKVLTG..........YMFMRAVNTAKKSRLTDVTL 199

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched:      650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters:      650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :     Issued_Patents_AA:*
               1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
               2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
               3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
               4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
               5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
               6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
               7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.

                            SUMMARIES
                   %
Result          Query
   No.   Score  Match Length DB  ID                         Description
```

SCORE Search Results Details for Application 10723602 and Search Result us-10-723-602-2.ra

This page gives you Search Results detail for the Application 10723602 and Search Result us-10-7.
2.rapbm.

start

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```
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OM protein - protein search, using sw model

Run on:          May 26, 2006, 11:28:37 ; Search time 296.12 Seconds
                                          (without alignments)
                                          311.292 Million cell updates/sec

Title:           US-10-723-602-2
Perfect score:   1082
Sequence:        1 MKSGLWYFFLFCLRIKVLTG..........YMFMRAVNTAKKSRLTDVTL 199

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters:     2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Published_Applications_AA_Main:*
                 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
                 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
                 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
                 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
                 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
                 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.

                              SUMMARIES
                       %
Result              Query
   No.   Score  Match Length DB  ID                      Description
------------------------------------------------------------------------
     1    1082  100.0    199   3  US-09-833-245-113       Sequence 113, App
     2    1082  100.0    199   3  US-09-833-245-114       Sequence 114, App
     3    1082  100.0    199   4  US-10-107-828-2         Sequence 2, Appli
```

SCORE Search Results Details for Applicatior 10723602 and Search Result us-10-723-602-2.ra

This page gives you Search Results detail for the Application 10723602 and Search Result us-10-7. 2.rapbn.

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OM protein - protein search, using sw model

Run on:        May 26, 2006, 11:30:16 ; Search time 17.1388 Seconds
                                       (without alignments)
                                       129.317 Million cell updates/sec

Title:         US-10-723-602-2
Perfect score: 1082
Sequence:      1 MKSGLWYFFLFCLRIKVLTG..........YMFMRAVNTAKKSRLTDVTL 199

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched:      56051 seqs, 11137335 residues

Total number of hits satisfying chosen parameters:      56051

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :     Published_Applications_AA_New:*
               1:  /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
               2:  /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
               3:  /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
               4:  /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
               5:  /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
               6:  /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
               7:  /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
               8:  /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1082	100.0	199	6	US-10-511-937-2440	Sequence 2440, Ap

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This page gives you Search Results detail for the Application 10723602 and Search Result us-10-7.
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```
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```

OM protein - protein search, using sw model

```
Run on:        May 26, 2006, 11:19:42 ; Search time 55.2249 Seconds
                                        (without alignments)
                                        346.712 Million cell updates/sec
```

```
Title:          US-10-723-602-2
Perfect score:  1082
Sequence:       1 MKSGLWYFFLFCLRIKVLTG..........YMFMRAVNTAKKSRLTDVTL 199
```

```
Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5
```

```
Searched:       283416 seqs, 96216763 residues
```

Total number of hits satisfying chosen parameters: 283416

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries
```

```
Database :      PIR_80:*
                1:  pir1:*
                2:  pir2:*
                3:  pir3:*
                4:  pir4:*
```

```
         Pred. No. is the number of results predicted by chance to have a
         score greater than or equal to the score of the result being printed,
         and is derived by analysis of the total score distribution.
```

                                SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1082	100.0	199	2	S78540	inducible T-cell c
2	701	64.8	200	2	JC7397	activation-inducib
3	696	64.3	216	2	JC7396	activation-inducib
4	152	14.0	218	2	S24413	T-cell surface gly
5	150.5	13.9	221	2	I46689	CD28 precursor - r
6	139.5	12.9	173	2	I46197	cell surface prote
7	139.5	12.9	220	1	RWHU28	T-cell surface gly
8	138	12.8	218	2	A43523	T-cell surface gly

SCORE Search Results Details for Application 10723602 and Search Result us-10-723-602-2.rup.

<u>Score Home Page</u>	<u>Retrieve Application List</u>	<u>SCORE System Overview</u>	<u>SCORE FAQ</u>	<u>Comments / Suggestions</u>

This page gives you Search Results detail for the Application 10723602 and Search Result us-10-723-602-2.rup.

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```
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OM protein - protein search, using sw model

Run on:        May 26, 2006, 11:11:46 ; Search time 453.225 Seconds
                                         (without alignments)
                                         406.152 Million cell updates/sec

Title:         US-10-723-602-2
Perfect score: 1082
Sequence:      1 MKSGLWYFFLFCLRIKVLTG..........YMFMRAVNTAKKSRLTDVTL 199

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched:      2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters:      2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :     UniProt_7.2:*
               1:  uniprot_sprot:*
               2:  uniprot_trembl:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                            SUMMARIES
                    %
Result          Query
   No.   Score   Match Length DB  ID                        Description
   ---------------------------------------------------------------------------
        1    1082   100.0    199  1   ICOS_HUMAN               Q9y6w8 homo sapien
        2    1082   100.0    199  2   Q53QY6_HUMAN             Q53qy6 homo sapien
        3    804.5   74.4    209  2   Q2KMN0_PIG               Q2kmn0 sus scrofa
        4    788.5   72.9    209  1   ICOS_BOVIN               Q58df9 bos taurus
```